

FIG. 1

2/21

LINKER #1 15bp | SV40 ORIGIN=332bp
GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGCTGG GGAGCCTGGG 240
GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAAT TAATCCCCT 360
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTTG 480
CMV PROMOTER-ENHANCER=567bp
ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTG TGCCAGTAC 660
ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
Bgl II | LINKER #3=76bp | LEADER=60bp
CATCACAGAT CTCTCACCAT GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1140
TGCTGCTGA ATAATTCTA TCCAGAGAG GCCAAAGTAC AGTGAAGGT GGATAACGCC 1200
HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
CTCCAATCGG GTAACCTCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380
STOP
LIGHT CHAIN | Eco RI | LINKER #4=85bp
TGTTCAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCGT GACAACATGC 1440
GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500

FIG. 2A

3/21

GTTCGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1560
TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 1740
ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 1800
TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860
GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCAGG GGGATTTCAC AGTCTCCACC 1920
CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980
GTAACAAC TC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCCGAC 2100
ATGGGTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACGCGTGT CGCTAGCACC 2160
START HEAVY CHAIN
AAGGGCCCCAT CCGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220
GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA 2280
GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
GACAAAAC TC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
TTCCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGT CACA 2580
TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGA CTACAA 2760
TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAGG 2880
AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

4/21

GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
STOP HEAVY CHAIN |Bam HI **LINKER #7=81bp**
CTCTCCCTGT CTCCGGGTAA ATGAGGATCC GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
3144 15
TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC CTCGACTGTG CTTTCTAGTT 3240
3225 16
GCCAGCCATC TGTGTTTTGC CCCTCCCCCG TGCCTTCCTT GACCCTGGAA GGTGCCACTC 3300
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
CCACTGTCCT TTCCTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATACCA 3420
GGCATGCTGG GGATGCGGTG GGCTCTATGG AACCAGCTGG GGCTCGACAG CGCTGGATCT 3480
3456 17
CCCGATCCCC AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 3540
3490 1
AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 3840
CTGACATAGT TGTGTTGGGA GCTTGGATAG CTTGACAGC TCAGGGCTGC GATTTGCGGC 3900
3856 7 3875 16
CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC TGCCATCAT 3960
3957 18
GTTCGACCAT TGAAGTGCAT CGTCGCCGTG TCCCAAAATA TGGGGATTGG CAAGAACGGA 4020
GACCTACCCT GGCCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAACC 4080
TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGGTA GGAAACCTG GTTCTCCATT 4140
MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200
GAACCACCAC GAGGAGCTCA TTTTCTTGCC AAAAGTTTGG ATGATGCCTT AAGACTTATT 4260
GAACAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTTGGG TAGTCGGAGG CAGTTCTGTT 4320
TACCAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
GAATTTGAAA GTGACACGTT TTTCCAGAA ATTGATTTGG GGAAATATAA ACTTCTCCCA 4440
GAATACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTTGAA 4500

FIG. 2C

5/21

STOP DHFR
 GTCTACGAGA AGAAAGAC TA ACAGGAAGAT GCTTTCAAGT TCTCTGCTCC CCTCCTAAAG 4560
 4521 2
 3' UNTRANSLATED DHFR=82bp LINKER #10=10bp
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTTT AGATCAGCCT CGACTGTGCC 4620
 4603 4 4613 4
 TTCTAGTTGC CAGCCATCTG TTGTTTGGCC CTCCCCCGTG CCTTCCTTGA CCCTGGAAGG 4680
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740
 GTGTCATTCT ATTCTGGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860
 4844 5
 TAGCTTTGCT TCTCAATTC TTATTTGCAT AATGAGAAAA AAAGGAAAAAT TAATTTTAAC 4920
 ACCAATTCAG TAGTTGATTG AGCAAATGCG TTGCCAAAAA GGATGCTTTA GAGACAGTGT 4980
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040
 GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATTC 5100
 CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160
 AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTTGCT TCTGACATAG 5220
 LINKER #12=21bp START NEO
 TTGTGTTGGG AGCTTGGATC GATCCTCTAT GGTGAACAA GATGGATTGC ACGCAGGTTC 5280
 5227 8 5248 9
 TCCGGCCGCT TGGGTGGAGA GGCTATTCGG CTATGACTGG GCACAACAGA CAATCGGCTG 5340
 CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGGCG CCGGTTCTTT TTGTCAAGAC 5400
 NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAAGTGA GGACGAGGCA GCGEGGCTAT CGTGGCTGGC 5460
 795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520
 GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTTG CTCCTGCCGA 5580
 GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640
 CCCATTCGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGAAGCCGG 5700
 TCTTGTCGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760
 CGCCAGGCTC AAGGCGCGCA TGCCCGACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820
 CTGCTTGCCG AATATCATGG TGGAAAATGG CCGCTTTTCT GGATTCATCG ACTGTGGCCG 5880
 GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940
 GCTTGGCGGC GAATGGGCTG ACCGCTTCCT CGTGCTTTAC GGTATCGCCG CTCCCGATTG 6000

FIG. 2D

6/21

GCAGCGCATC GCCTTCTATC GCCTTCTTGA CGAGTTCTTC ^{STOP NEO} TGAGCGGGGAC TCTGGGGTTC 6060
 6043 4
 GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCACGAG ATTTTCGATTC CACCGCCGCC 6120
 TTCTATGAAA GGTGCGGCTT ^{3' UNTRANSLATED NEO=173bp} CGGAATCGTT TTCCGGGACG CCGGCTGGAT GATCCTCCAG 6180
 CGCGGGGATC TCATGCTGGA GTTCTTCGCC CACCCCAACT ^{6216 7} TGTTTATTGC AGCTTATAAT 6240
 GGTTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TTCACTGCAT 6300
 TCTAGTTGTG GTTTGTCCAA ^{SV40 POLY A EARLY=133bp} ACTCATCAAT CTATCTTATC ^{LINKER #13=19bp} ATGTCTGGAT ^{6349 50} CGCGGCCGCG 6360
 ATCCCGTGA ^{6368 9} GAGCTTGGCG TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTTATC 6420
 CGCTCACAAT TCCACACAAC ATACGAGCCG GAAGCATAAA GTGTAAAGCC TGGGGTGCCT 6480
 AATGAGTGAG CTAATCACA TTAATTGCGT TCGGCTCACT GCGCGCTTTC CAGTCGGGAA 6540
 ACCTGTCGTG CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA 6600
 TTGGGCGCTC TTCCGCTTCC ^{PVC 19} TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660
 GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG 6720
 CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT 6780
 TGCTGGCGTT ^{6792=BACTERIAL ORIGIN OF REPLICATION} TTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840
 GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATACCA GCGGTTTCCC CCTGGAAGCT 6900
 CCCTCGTGCG CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC 6960
 CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020
 TCGTTCGCTC CAAGCTGGGC TGTGTGCACG AACCCCCCGT TCAGCCCGAC CGCTGCGCCT 7080
 TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG 7140
 CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CCGTGCTACA GAGTTCTTGA 7200
 AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260
 AGCCAGTTAC CTTCCGAAAA AGAGTTGGTA GCTCTTGATC CGGCAACAA ACCACCGCTG 7320
 GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC AGATTACCGC CAGAAAAAAA GGATCTCAAG 7380
 AAGATCCTTT GATCTTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAC TCACGTTAAG 7440
 GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTACCTA GATCCTTTTA AATTAAAAAT 7500

FIG. 2E

7/21

GAAGTTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT 7560
TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTTCG TTCATCCATA GTTGCCTGAC 7620
TCCCCGTCGT GTAGATAACT ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTTATC AGCAATAAAC CAGCCAGCCG 7740
GAAGGGCCGA GCGCAGAAGT GGTCTTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800
GTTGCCGGGA AGCTAGAGTA AGTAGTTTCG CAGTTAATAG TTTGCGCAAC GTTGTGCGCA 7860
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC AGCTCCGGTT 7920
CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCCT 7980
TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040
CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG 8100
AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCCG 8160
CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCCGATG 8280
AACCCTACTG TGCACCCAAC TGATCTTCAG CATCTTTTAC TTTCACCAGC GTTTCTGGGT 8340
GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT 8520
TTCCCCGAAA AGTGCCACCT

FIG. 2F

8/21

LINKER #1=15bp
GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
15 6

AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120

SV40 ORIGIN=332bp
GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180

ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240

GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300

GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAAT TAATTCCTCT 360
347 8

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420

GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTTG 480

ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540

CVM PROMOTER-ENHANCER=567bp
TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600

AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC CCTGGCATTG TGCCCACTAC 660

ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720

ATGGTGATGC GGTGTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780

TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840

GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900

CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
927 8 934 5

LINKER #3=7bp

Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp
CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT 1020
978 9

GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
1044 5+1

GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTGAAGTGT AAGTTACATC 1140

CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCT GGATTTATGC CACATCCAAC 1200

LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID
CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TACTCTCTC 1260

ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320

AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
1362 3

TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG 1440

TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1500

FIG. 3A

9/21

HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAAC TCCCA GGAGAGTGTG ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
 AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=81bp
 TGTTCGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACA TGC 1740
 1646 7
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
 1771 2
 GTTTGCCCCCT CCCCCGTGCC TTCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1860
 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
 GCGGTGGGCT CTATGGAACC AGCTGGGGCT CGACAGCTAT GCCAAGTACG CCCCTATTG 2040
 2002 3 2017 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCCA GTACATGACC TTATGGGACT 2100
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 2160
 CMV PROMOTER-ENHANCER=334bp
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 2220
 CCATTGACGT CAATGGGAGT TTGTTTTGGC ACCAAAATCA ACGGGACTTT CAAAATGTC 2280
 GTAACAAC TC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGACGGTGG GAGGTCTATA 2340
 LINKER #6=7bp Sal I
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
 2351 2 2358 9
 START
 HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457 8
 ATGGGTTGGA GCCTCATCTT GCTCTTCCTT GTCGCTGTTG CTACCGGTGT CCTGTCCGAG 2460
 2401 -5 -4 -3 -2 -1 +1
 GTACAAC TGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
 TGCAAGGCTT CTGGCTACAC ATTTACCAGT TACAATATGC ACTGGGTAAA ACAGACACCT 2580
 HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
 GGTCGGGGCC TGGAAATGGAT TGGAGCTATT TATCCCGGAA ATGGTGATAC TTCCTACAAT 2640
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
 TACGGCGGTG ACTGGTACTT CAATGTCTGG GGCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
 Nhe I
 GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 2880
 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGG 2940
 HUMAN GAMMA 1 CONSTANT=993bp
 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 3000

FIG. 3B

10/21

330 AMINO ACID & STOP CODON
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3260
TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
AAATCTTGTG ACAAACCTCA CACATGCCCA CCGTGCCAG CACCTGAACT CCTGGGGGGA 3180
CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
GAGGTACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
AGCACGTACC GTGTGGTCAG CGTCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480
AAAGCCAAAG GGCAGCCCCG AGAACCACAG GTGTACACCC TGCCCCATC CCGGGATGAG 3540
CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAAC ACAAGACCAC GCCTCCCGTG 3660
CTGGACTCCG ACGGCTCCTT CTTCCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
CAGAAGAGCC TCTCCCTGTC TCCGGGTAAA TGAGGATCCG TTAACGGTTA CCAACTACCT 3840
AGACTGGATT CGTGACAACA TGCGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900
CTTCTAGTTG CCAGCCATCT GTTGTITGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG 3960
GTGCCACTCC CACTGTCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020
BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
GGTGTCAATC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080
ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140
GCTGGATCTC CCGATCCCA GCTTTGCTC TCAATTCTT ATTTGCATAA TGAGAAAAAA 4200
AGGAAAATTA ATTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
ATGCTTTAGA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTCAG AGGGAGTACC 4320
CAGAGCTGAG ACTCCTAAGC CAGTGAGTGG CACAGCATTC TAGGGAGAAA TATGCTTGTC 4380
ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCCAATCTG CTCACACAGG 4440
ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTCA 4500

FIG. 3C

11/21

CATTGCTTC TGACATAGTT **LINKER #9=19bp** **5' UNTRANSLATED DHFR=82bp**
 GTGTTGGGAG CTTGGATAGC TTGGACAGCT CAGGGCTGCC 4560
 4525 6 4544 5
 ATTCGCGCC AAACCTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620
START DHFR
 GCCATCATCG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
 4626 7
 AGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
 ACCACAACCT CTTCACTGGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800
DHFR=564bp=187 AMINO ACID & STOP CODON
 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA TGATGCCTTA 4920
 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTTGGG GAAATATAAA 5100
 CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
STOP DHFR **3' UNTRANSLATED DHFR=82bp**
 AAGTTTGAAG TCTACGAGAA GAAAGAC TAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220
 5140 1
 CTCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA **LINKER #10**
 5272 3
=10bp
 GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC TCCCCCGTGC CTTCTTGAC 5340
BOVINE GROWTH HORMONE POLYADENYLATION=231bp
 CCTGGAAGGT GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATTG 5400
 TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
LINKER #11
 TTGGAAGAC AATAGCAGGC ATGCTGGGGA TCGGGTGGGC TCTATGGAAC **CAGCTGGGGC** 5520
 5513 4
=17bp
 TCGAGCTACT AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAATT 5580
 5530 1
 AATTTTAAAC CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCGAA 5700
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880
LINKER #12=21bp **START NEO**
 CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
 5896 7 5917 8
 CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTCGSC TATGACTGGG CACAACAGAC 6000

FIG. 3D

12/21

AATCGGCTGC TCTGATGCCG CCGTGTTCCG GCTGTCAGCG CAGGGGGCGC CGGTTCTTTT 6060
NEOMYCIN PHOSPHOTRANSFERASE=795bp=264 AMINO ACID & STOP CODON
 TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAAGTGCAG GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTGAT CTCACCTTGC 6240
 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCCG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTT GCCAGGCTCA AGGCGCGCAT GCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTTCATGA 6540
 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATTAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCTC GTGCTTTACG GTATCGCCGC 6660
 TCCCGATTCT CAGCGCATCG CTTTCTATCG CTTTCTTGA CAGTTCTTCT **STOP NEO** 6720
 6712 3
 CTGGGGTTCT AAATGACCGA CCAAGCGACG CCCAACCTGC CATCAGGAGA TTTCGATTCC 6780
 ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
 ATCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCC ACCCCAACTT GTTTATTGCA 6900
 6885 6
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAATT TCACAAATA AGCATTTTTT 6960
 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
 7018 9
LINKER #13=19bp
 GCGGCCGCGA TCCCGTCCAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
 7037 8
PUC 19
 ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCCG AAGCATAAAG TGTAAGCCCT 7140
 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTTC 7200
 AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260
 GTTTGCGTAT TGGGCGCTCT TCCGCTTCTT CGCTCACTGA CTCGCTGCGC TCGGTCGTTT 7320
 GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG 7380
 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA 7440
 7461=BACTERIAL ORIGIN OF REPLICATION
 AGGCCGCGTT GCTGGCGTTT TCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC 7500

FIG. 3E

13/21

GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
 CGGTGTAGGT CGTTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAAACAAA 7980
 CCACCGCTGG TAGCGGTGGT TTTTTTGTTC GCAAGCAGCA GATTACGCGC AGAAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT 8100
 CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTACCTAG ATCCTTTTAA 8160
 ATAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT STOP 8220
BETA LACTAMASE
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280
 TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC 8400
 BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
 AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCCGC AGTTAATAGT TTGCCAACG 8520
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580
 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
 TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCACTG TTATCACTCA 8700
 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760
 TGA CTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT 8820
 CTTGCCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GGTGATGTA ACCCACTCGT GCACCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000
 TTTCTGGGTG AGCAAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCATA START BETA LACTAMASE CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

[illegible][illegible]

FIG. 4

15/21

LEADER

-19	-15	-10	-5
FRAME 1 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val			
ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC			
2409	2418	2427	2436 2445
-1	+1	FR1	10
Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Ala Gly Ala Ser			
CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG GCC TCA			
2460	2469	2478	2487 2496 2505
20	25	30	31 CDR1 35 36
Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp			
GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC AAT ATG CAC TGG			
2517	2526	2536	2544 2553 2562
40	FR2	45	49 50 52 52A 53 54
Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn			
GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA GCT ATT TAT CCC GGA AAT			
2574	2583	2592	2601 2610 2615
55	CDR2	60	65 66 FR3 70
Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys			
GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC AAG GCC ACA TTG ACT GCA GAC AAA			
2631	2640	2649	2658 2667 2676
75	80	82	82A 82B 82C 83 85
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val			
TCC TCC AGC ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT CAG GAC TCT GCG GTC			
2688	2697	2706	2715 2724 2733
90	94	95	CDR3 100 100A 100B 100C 100D 101 102 103
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly			
TAT TAC TGT GCA AGA TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC			
2745	2754	2763	2772 2781 2790
105	FR4	110	113
Ala Gly Thr Thr Val Thr Val Ser Ala			
GCA GGG ACC ACG GTC ACC GTC TCT GCA			
2802	2811	2820	

FIG. 5

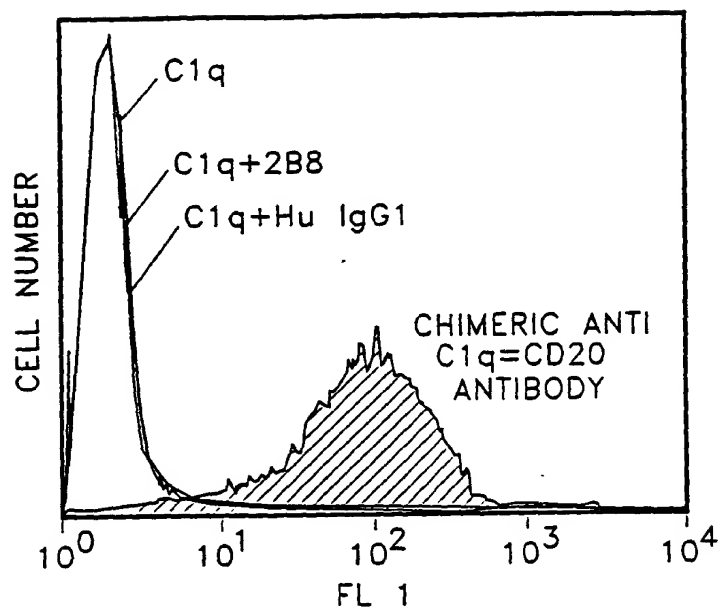


FIG. 6

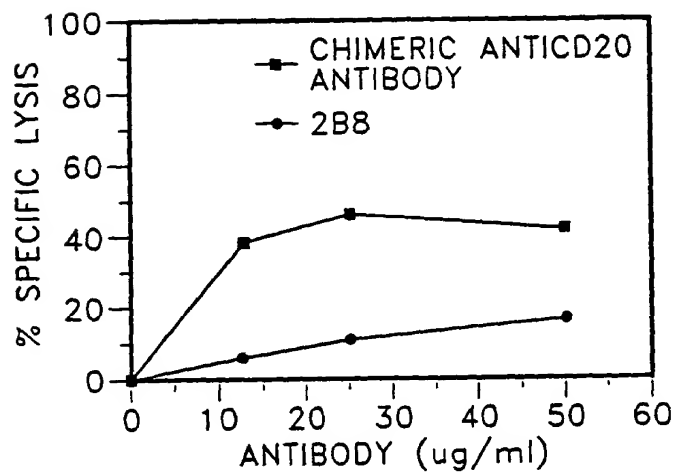
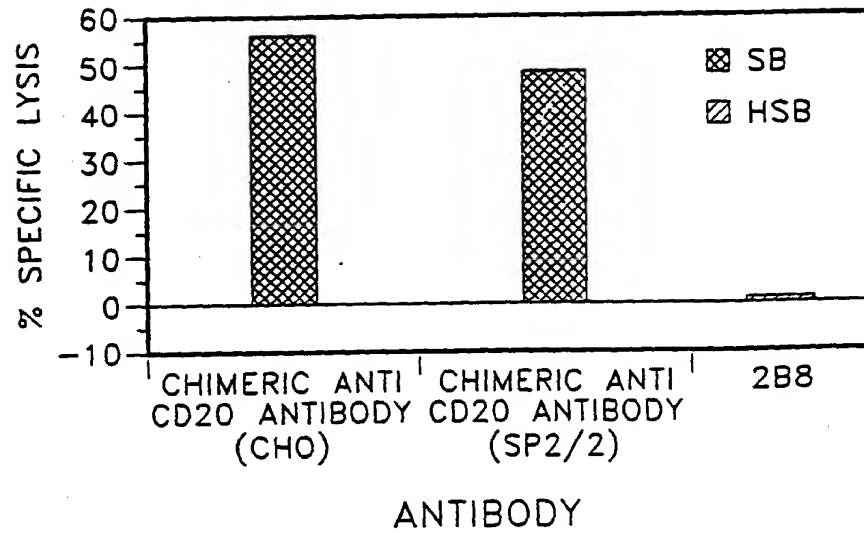
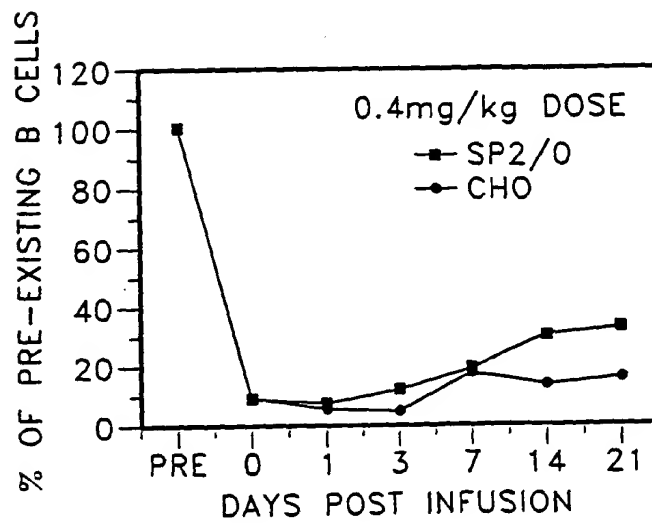
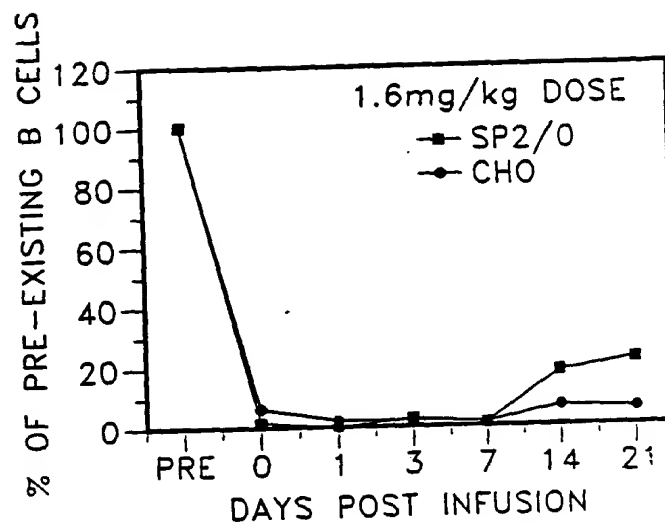
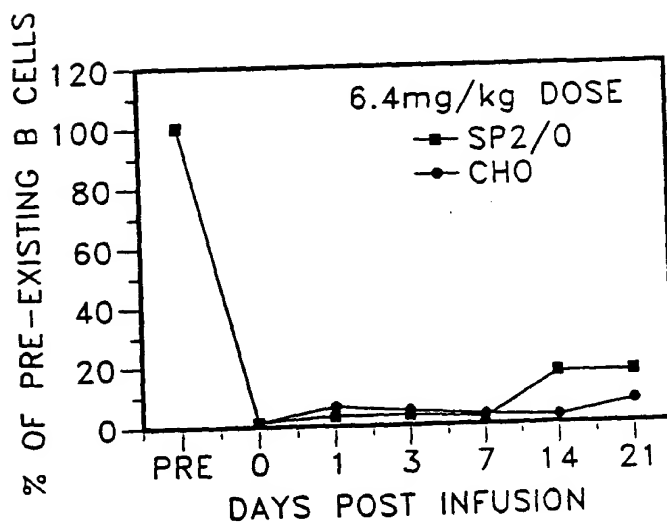
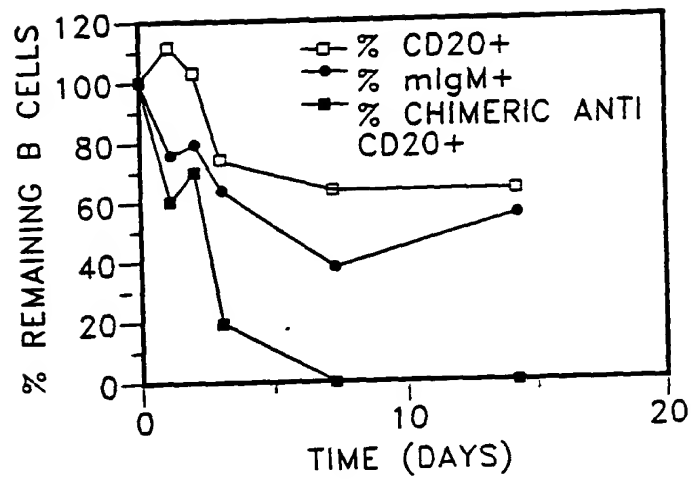
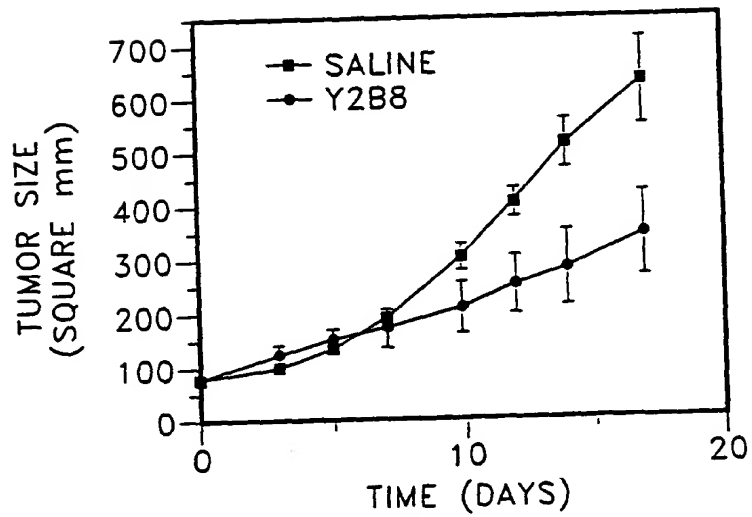
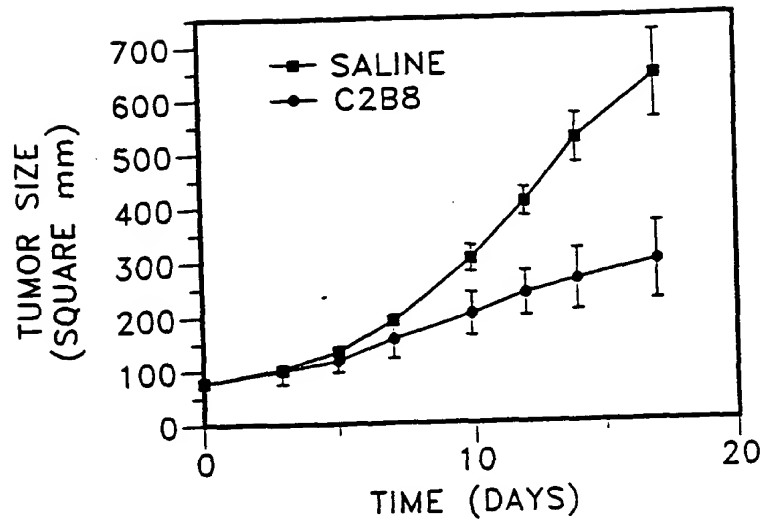
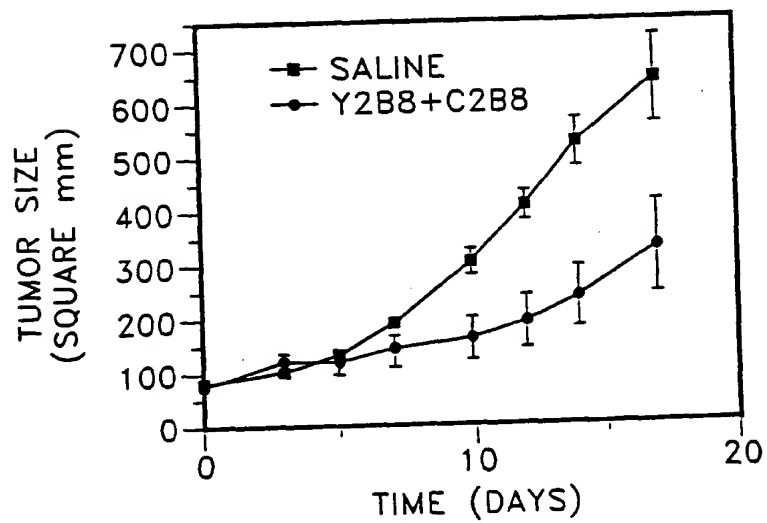


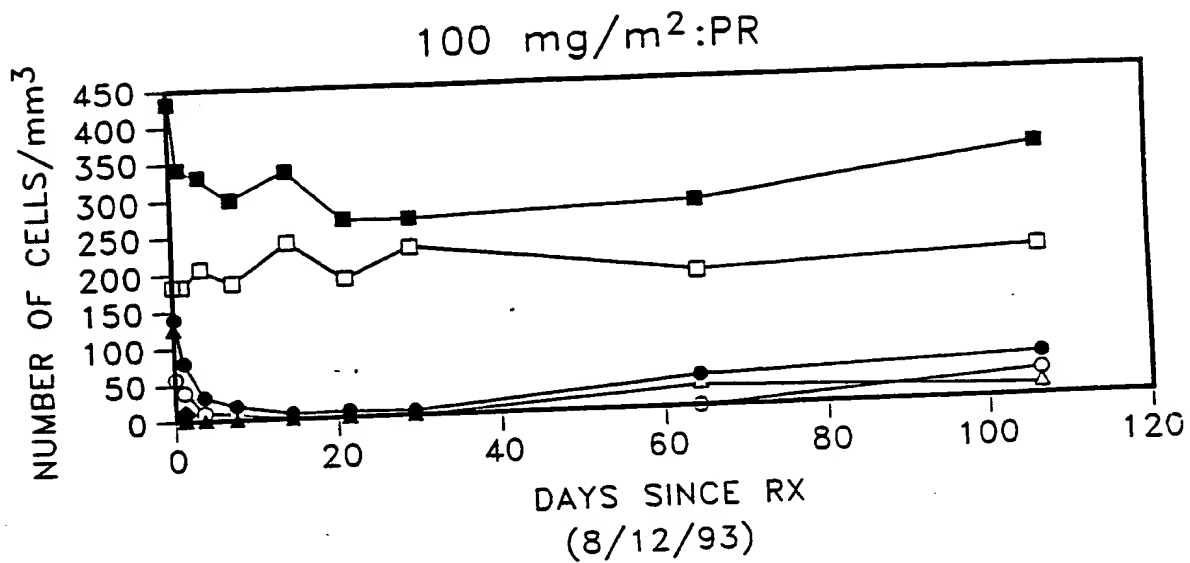
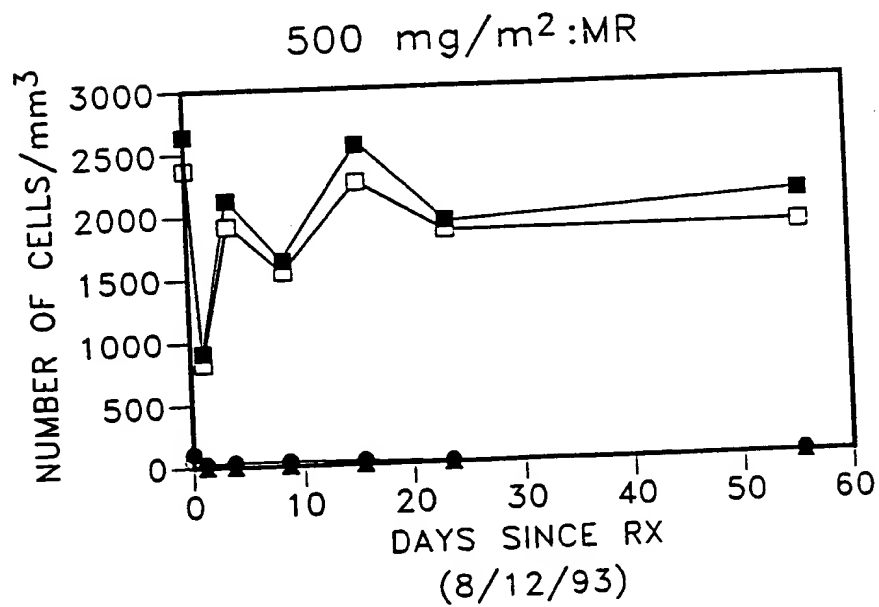
FIG. 7

*FIG. 8**FIG. 9A*

*FIG. 9B**FIG. 9C*

*FIG. 10**FIG. 11*

*FIG. 12**FIG. 13*

*FIG. 14A**FIG. 14B*